

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: Mixson, James A

(ii) TITLE OF INVENTION: CARRIER:NUCLEIC ACIDS COMPLEXES CONTAINING  
NUCLEIC ACIDS ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN  
GENE THERAPY

(iii) NUMBER OF SEQUENCES: 43

#### (iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Wilmington

(D) STATE: Delaware

(E) COUNTRY: U.S.A.

(F) ZIP: 19899

#### (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk (provided in parent application)

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

#### (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Not yet assigned

(B) FILING DATE:

(C) CLASSIFICATION:

#### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/985,526

(B) FILING DATE: 5-DEC-1997

#### (viii) ATTORNEY/AGENT INFORMATION:

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#### (ix) TELECOMMUNICATION INFORMATION:

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### (2) INFORMATION FOR SEQ ID NO:1:

1003669.12901

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro  
1 5 10 15

Leu Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr  
20 25 30

Val Asp Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys  
35 40 45

Lys Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro  
50 55 60

Asp Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp  
65 70 75 80

Gly Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly  
85 90 95

Asn Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg  
100 105 110

Cys Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys  
115 120 125

Asp Lys Arg Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp  
130 135 140

Ser Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr  
145 150 155 160

Asn Leu Cys Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly  
165 170 175

Arg Glu Ala Glu Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn

180

185

190

Gly Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys  
 195 200 205

Gly Gly Gly Val Gln Lys Arg Ser Arg Leu  
 210 215

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGACTGAAG AGAACAAAGA GTTGGCCAAT GAGCTGAGGC GGCCTCCCCT  
 ATGCTATCAC 60

AACGGAGTTC AGTACAGAAA TAACGAGGAA TGGACTGTTG ATAGCTGCAC  
 TGAGTGTCAC 120

TGTCAGAACT CAGTTACCAT CTGCAAAAAG GTGTCCTGCC CCATCATGCC  
 CTGCTCCAAT 180

GCCACAGTTC CTGATGGAGA ATGCTGTCCT CGCTGTTGGC CCAGCGACTC  
 TGCGGACGAT 240

GGCTGGTCTC CATGGTCCGA GTGGACCTCC TGTTCTACGA GCTGTGGCAA  
 TGGAATTCAG 300

CAGCGCGGCC GCTCCTGCGA TAGCCTCAAC AACCGATGTG AGGGCTCCTC  
 GTCCAGACA 360

CGGACCTGCC ACATTCAGGA GTGTGACAAA AGATTAAAC AGGATGGTGG  
 CTGGAGCCAC 420

TGGTCCCCGT GGTCACTTG TTCTGTGACA TGTGGTGATG GTGTGATCAC  
 AAGGATCCGG 480

CTCTGCAACT CTCCCAGCCC CCAGATGAAT GGGAAACCCT GTGAAGGCGA  
AGCGCGGGAG 540

ACCAAAGCCT GCAAGAAAGA CGCCTGCCCC ATCAATGGAG GCTGGGGTCC  
TTGGTCACCA 600

TGGGACATCT GTTCTGTCAC CTGTGGAGGA GGGGTACAGA AACGTAGTCG  
TCTCTAA 656

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro  
1 5 10 15

Leu Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr  
20 25 30

Asp Val Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys  
35 40 45

Lys Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro  
50 55 60

Asp Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp  
65 70 75 80

Trp Gly Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly  
85 90 95

Gly Asn Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg  
100 105 110

Cys Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys  
115 120 125

Asp Lys Arg Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp  
130 135 140

Ser Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr  
145 150 155 160

Leu Cys Asn Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly  
165 170 175

Glu Ala Arg Glu Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn  
180 185 190

Gly Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys  
195 200 205

Gly Gly Gly Val Gln Lys Arg Ser Arg Leu Cys Val Asp Ser Arg Met  
210 215 220

Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu  
225 230 235 240

Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val  
245 250 255

Asp Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys  
260 265 270

Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp  
275 280 285

Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly  
290 295 300

Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn  
305 310 315 320

Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys  
325 330 335

Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp  
340 345 350

Lys Arg Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser  
355 360 365

Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr Leu  
370 375 380

Cys Asn Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu  
385 390 395 400

Ala Arg Glu Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly  
405 410 415

Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly  
420 425 430

Gly Gly Val Gln Lys Arg Ser Arg Leu  
435 440

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGACTGAAG AGAACAAAGA GTTGGCCAAT GAGCTGAGGC GGCCTCCCCT  
ATGCTATCAC 60

AACGGAGTTC AGTACAGAAA TAACGAGGAA TGGACTGTTG ATAGCTGCAC  
TGAGTGTAC 120

TGTCAGAACT CAGTTACCAT CTGCAAAAAG GTGTCCTGCC CCATCATGCC  
CTGCTCCAAT 180

GCCACAGTTC CTGATGGAGA ATGCTGTCCT CGCTGTTGGC CCAGCGACTC  
TGCGGACGAT 240

GGCTGGTCTC CATGGTCCGA GTGGACCTCC TGTTCTACGA GCTGTGGCAA  
TGGAATTCAG 300

CAGCGCGGCC GCTCCTGCGA TAGCCTCAAC AACCGATGTG AGGGCTCCTC

GGTCCAGACA 360

CGGACCTGCC ACATTCAGGA GTGTGACAAA AGATTAAAC AGGATGGTGG  
CTGGAGCCAC 420

TGGTCCCCGT GGTTCATCTTG TTCTGTGACA TGTGGTGATG GTGTGATCAC  
AAGGATCCGG 480

CTCTGCAACT CTCCCAGCCC CCAGATGAAT GGGAAACCCT GTGAAGGCGA  
AGCGCGGGAG 540

ACCAAAGCCT GCAAGAAAGA CGCCTGCCCC ATCAATGGAG GCTGGGGTCC  
TTGGTCACCA 600

TGGGACATCT GTTCTGTCAC CTGTGGAGGA GGGGTACAGA AACGTAGTCG  
TCTCTGCGTC 660

GACTCTAGAA TGAAGTGAAGA GAACAAAGAG TTGGCCAATG AGCTGAGGCG  
GCCTCCCCTA 720

TGCTATCACA ACGGAGTTCA GTACAGAAAT AACGAGGAAT GGACTGTTGA  
TAGCTGCACT 780

GAGTGTCACT GTCAGAACTC AGTTACCATC TGCAAAAAGG TGTCTGCCCC  
CATCATGCCC 840

TGCTCCAATG CCACAGTTCC TGATGGAGAA TGCTGTCCTC GCTGTTGGCC  
CAGCGACTCT 900

GCGGACGATG GCTGGTCTCC ATGGTCCGAG TGGACCTCCT GTTCTACGAG  
CTGTGGCAAT 960

GGAATTCAGC AGCGCGGCCG CTCCTGCGAT AGCCTCAACA ACCGATGTGA  
GGGCTCCTCG 1020

GTCCAGACAC GGACCTGCCA CATTGAGGAG TGTGACAAAA GATTAAACA  
GGATGGTGGC 1080

TGGAGCCACT GGTCCCCGTG GTCATCTTGT TCTGTGACAT GTGGTGATGG  
TGTGATCACA 1140

AGGATCCGGC TCTGCAACTC TCCCAGCCCC CAGATGAATG GGAAACCCTG  
TGAAGGCGAA 1200

GCGCGGGAGA CCAAAGCCTG CAAGAAAGAC GCCTGCCCCA TCAATGGAGG

CTGGGGTCCT 1260

TGGTCACCAT GGGACATCTG TTCTGTCACC TGTGGAGGAG GGGTACAGAA  
ACGTAGTCGT 1320

CTCTAA

1326

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Tyr Ile Gly Ser Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTCGACATGT ATATTGGTTC TCGTTAAGTC GAC

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear



[illegible]

Ser Tyr Ile Gly Ser Arg Gly Lys Ser  
20 25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

GTCGACATGT ATATTGGTTC TCGTGTA AAA GTTATATTGG TTCTCGTGGT  
AAAAGTTATA 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) **SEQUENCE CHARACTERISTICS:**  
 (A) **LENGTH:** 13 amino acids  
 (B) **TYPE:** amino acid  
 (D) **TOPOLOGY:** linear

Met Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCGACATGC TTTATAAGAA GATCATCAAG AAGCTTCTTG AGAGTTAAGT CGAC  
54

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser  
1            5            10            15

Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser Leu  
20            25            30

Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser  
35            40            45

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCGACATGC TTTATAAGAA GATCATCAAG AAGCTTCTTG AGAGTGGTAA  
AAGTCTTTAT 60

AAGAAGATCA TCAAGAAGCT TCTTGAGAGT GGTAAGAGTC TTTATAAGAA  
GATCATCAAG 120

AAGCTTCTTG AGAGTGGTAA AAGTTAAGTC GAC

153

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Phe Cys Tyr Trp Lys Val Cys Trp

1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTCGACATGT TCTGTTATTG GAAGGTTTGT TGGTAAGTCG AC

42

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Phe Cys Tyr Trp Lys Val Cys Trp Gly Lys Ser Phe Cys Tyr Trp  
1            5            10            15

Lys Val Cys Trp Gly Lys Ser Phe Cys Tyr Trp Lys Val Cys Trp Gly  
20            25            30

Lys Ser

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCGACATGT TCTGTTATTG GAAGGTTTGT TGGGGTAAAA GTTTCTGTTA  
TTGGAAGGTT    60

TGTTGGGGTA AAAGTTTCTG TTATTGGAAG GTTTGTTGGG GTAAAAGTTA  
AGTCGAC    117

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Gly Arg Gly Asp

1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTCGACATGG GTCGTGGTGA TTAAGTCGAC

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly Arg Gly Asp Gly Lys Ser Gly Arg Gly Asp Gly Lys Ser Gly

1 5 10 15

Arg Gly Asp Gly Lys Ser  
20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTCGACATGG GTCGTGGTGA TGGTAAAAGT GGTCGTGGTG ATGGTAAAAG  
TGGTCGTGGT 60

GATGGTAAAA GTTAAGTCGA C 81

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg  
1 5 10 15

Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly  
20 25 30

Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn  
35 40 45

Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln

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50                      55                      60  
Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys  
65                      70                      75                      80  
Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys  
85                      90                      95  
Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Lys Asp Cys Gln Ala  
100                      105                      110  
Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe  
115                      120                      125  
Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu  
130                      135                      140  
Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr  
145                      150                      155                      160  
Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Pro Ser Pro Thr  
165                      170                      175  
Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser  
180                      185                      190  
Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro  
195                      200                      205  
His Arg  
210

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTCGACATGG TGTATCTGTC AGAATGTAAG ACCGGCATCG GCAACGGCTA  
CAGAGGAACC 60

ATGTCCAGGA CAAAGAGTGG TGTTGCCTGT CAAAAGTGGG GTGCCACGTT  
CCCCCACGTA 120

CCCAACTACT CTCCCAGTAC ACATCCCAAT GAGGGACTAG AAGAGAACTA  
CTGTAGGAAC 180

CCAGACAATG ATGAACAAGG GCCTTGGTGC TACTACTACAG ATCCGGACAA  
GAGATATGAC 240

TACTGCAACA TTCCTGAATG TGAAGAGGAA TGCATGTACT GCAGTGGAGA  
AAAGTATGAG 300

GGCAAAATCT CCAAGACCAT GTCTGGACTT GACTGCCAGG CCTGGGATTC  
TCAGAGCCCA 360

CATGCTCATG GATACATCCC TGCCAAATTT CCAAGCAAGA ACCTGAAGAT  
GAATTATTGC 420

CACAACCCTG ACGGGGAGCC AAGGCCCTGG TGCTTCACAA CAGACCCCAC  
CAAACGCTGG 480

GAATACTGTG ACATCCCCCG CTGCACAACA CCCCCGCCCC CACCCAGCCC  
AACCTACCAA 540

TGTCTGAAAG GAAGAGGTGA AAATTACCGA GGGACCGTGT CTGTCACCGT  
GTCTGGGAAA 600

ACCTGTCAGC GCTGGAGTGA GCAAACCCCT CATAGGTGAG TCGAC

644

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:



Met Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg  
1 5 10 15

Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly  
20 25 30

Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn  
35 40 45

Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln  
50 55 60

Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys  
65 70 75 80

Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys  
85 90 95

Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Lys Asp Cys Gln Ala  
100 105 110

Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe  
115 120 125

Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu  
130 135 140

Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr  
145 150 155 160

Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Ser Pro Thr  
165 170 175

Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser  
180 185 190

Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro  
195 200 205

His Arg Gly Lys Ser Met Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile  
210 215 220

Gly Asn Gly Tyr Arg Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala  
225 230 235 240

Cys Gln Lys Trp Gly Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro  
245 250 255

Ser Thr His Pro Asn Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro  
260 265 270

Asp Asn Asp Glu Gln Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys  
275 280 285

Arg Tyr Asp Tyr Cys Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr  
290 295 300

Cys Ser Gly Glu Lys Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly  
305 310 315 320

Lys Asp Cys Gln Ala Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr  
325 330 335

Ile Pro Ala Lys Phe Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His  
340 345 350

Asn Pro Asp Gly Glu Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr  
355 360 365

Lys Arg Trp Glu Tyr Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro  
370 375 380

Pro Pro Ser Pro Thr Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr  
385 390 395 400

Arg Gly Thr Val Ser Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp  
405 410 415

Ser Glu Gln Thr Pro His Arg  
420

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCGACATGG TGTATCTGTC AGAATGTAAG ACCGGCATCG GCAACGGCTA  
CAGAGGAACC 60

ATGTCCAGGA CAAAGAGTGG TGTTCCTGT CAAAAGTGGG GTGCCACGTT  
CCCCACGTA 120

CCCAACTACT CTCCCAGTAC ACATCCCAAT GAGGGACTAG AAGAGAACTA  
CTGTAGGAAC 180

CCAGACAATG ATGAACAAGG GCCTTGGTGC TACTACTACAG ATCCGGACAA  
GAGATATGAC 240

TACTGCAACA TTCCTGAATG TGAAGAGGAA TGCATGTACT GCAGTGGAGA  
AAAGTATGAG 300

GGCAAAATCT CCAAGACCAT GTCTGGACTT GACTGCCAGG CCTGGGATTC  
TCAGAGCCCA 360

CATGCTCATG GATACATCCC TGCCAAATTT CCAAGCAAGA ACCTGAAGAT  
GAATTATTGC 420

CACAACCCTG ACGGGGAGCC AAGGCCCTGG TGCTTCACAA CAGACCCAC  
CAAACGCTGG 480

GAATACTGTG ACATCCCCCG CTGCACAACA CCCCCGCCCC CACCCAGCCC  
AACCTACCAA 540

TGTCTGAAAG GAAGAGGTGA AAATTACCGA GGGACCGTGT CTGTCACCGT  
GTCTGGGAAA 600

ACCTGTCAGC GCTGGAGTGA GCAAACCCCT CATAGGGGTA AAAGTATGGT  
GTATCTGTCA 660

GAATGTAAGA CCGGCATCGG CAACGGCTAC AGAGGAACCA TGTCCAGGAC  
AAAGAGTGGT 720

GTTGCCTGTC AAAAGTGGGG TGCCACGTTC CCCCACGTAC CCAACTACTC  
TCCCAGTACA 780

CATCCCAATG AGGGACTAGA AGAGAACTAC TGTAGGAACC CAGACAATGA  
TGAACAAGGG 840

10036869.112901

CCTTGGTGCT ACACTACAGA TCCGGACAAG AGATATGACT ACTGCAACAT  
TCCTGAATGT 900

GAAGAGGAAT GCATGTACTG CAGTGGAGAA AAGTATGAGG GCAAAATCTC  
CAAGACCATG 960

TCTGGACTTG ACTGCCAGGC CTGGGATTCT CAGAGCCCAC ATGCTCATGG  
ATACATCCCT 1020

GCCAAATTTT CAAGCAAGAA CCTGAAGATG AATTATTGCC ACAACCCTGA  
CGGGGAGCCA 1080

AGGCCCTGGT GCTTCACAAC AGACCCCACC AAACGCTGGG AATACTGTGA  
CATCCCCCGC 1140

TGCACAACAC CCCC GCCCCC ACCCAGCCCA ACCTACCAAT GTCTGAAAGG  
AAGAGGTGAA 1200

AATTACCGAG GGACCGTGTC TGTCACCGTG TCTGGGAAAA CCTGTCAGCG  
CTGGAGTGAG 1260

CAAACCCCTC ATAGGTGAGT CGAC 1284

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Leu Pro Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu  
1 5 10 15

Arg Glu Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn  
20 25 30

Leu Ser Ser Glu Met Phe Ser Glu Phe Glu Lys Arg Tyr Thr His Gly  
35 40 45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu  
50 55 60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp  
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu  
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Gln Ala  
100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCGACATGT TGCCCATCTG TCCCGGCGGG GCTGCCCGAT GCCAGGTGAC  
CCTTCGAGAC 60

CTGTTTGACC GCGCCGTCGT CCTGTCCCAC TACATCCATA ACCTCTCCTC  
AGAAATGTTC 120

AGCGAATTCG ATAAACGGTA TACCCATGGC CGGGGGTTCA TTACCAAGGC  
CATCAACAGC 180

TGCCCACTT CTTCCCTTGC CACCCCCGAA GACAAGGAGC AAGCCCAACA  
GATGAATCAA 240

AAAGACTTTC TGAGCCTGAT AGTCAGCATA TTGCGATCCT GGAATGAGCC  
TCTGTATCAT 300

CTGGTCACGG AAGTACGTGG TATGCAAGAA GCCCCGGAGG CTATCCTATC

CAAAGCTGTA 360

GAGATTGAGG AGCAAACCAA ATAAGTCGAC

390

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Leu Pro Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu  
1 5 10 15

Arg Glu Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn  
20 25 30

Leu Ser Ser Glu Met Phe Ser Glu Phe Glu Lys Arg Tyr Thr His Gly  
35 40 45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu  
50 55 60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp  
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu  
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Gln Ala  
100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Gly Lys Ser  
115 120 125

Met Leu Pro Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu  
130 135 140

Arg Glu Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn

145            150            155            160  
 Leu Ser Ser Glu Met Phe Ser Glu Phe Glu Lys Arg Tyr Thr His Gly  
           165            170            175  
 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu  
           180            185            190  
 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp  
           195            200            205  
 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu  
           210            215            220  
 Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Gln Ala  
           225            230            235            240  
 Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys  
           245            250

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCGACATGT TGCCCATCTG TCCCGGCGGG GCTGCCCGAT GCCAGGTGAC  
 CCTTCGAGAC    60  
 CTGTTTGACC GCGCCGTCGT CCTGTCCCAC TACATCCATA ACCTCTCCTC  
 AGAAATGTTC    120  
 AGCGAATTCG ATAAACGGTA TACCCATGGC CGGGGGTTCA TTACCAAGGC  
 CATCAACAGC    180  
 TGCCACACTT CTTCCCTTGC CACCCCCGAA GACAAGGAGC AAGCCCAACA  
 GATGAATCAA    240

AAAGACTTTC TGAGCCTGAT AGTCAGCATA TTGCGATCCT GGAATGAGCC  
TCTGTATCAT 300

CTGGTCACGG AAGTACGTGG TATGCAAGAA GCCCCGGAGG CTATCCTATC  
CAAAGCTGTA 360

GAGATTGAGG AGCAAACCGG TAAAAGTATG TTGCCCATCT GTCCCGGCGG  
GGCTGCCCCA 420

TGCCAGGTGA CCCTTCGAGA CCTGTTTGAC CGCGCCGTCG TCCTGTCCCA  
CTACATCCAT 480

AACCTCTCCT CAGAAATGTT CAGCGAATTC GATAAACGGT ATACCCATGG  
CCGGGGGTTC 540

ATTACCAAGG CCATCAACAG CTGCCACACT TCTTCCCTTG CCACCCCCGA  
AGACAAGGAG 600

CAAGCCCAAC AGATGAATCA AAAAGACTTT CTGAGCCTGA TAGTCAGCAT  
ATTGCGATCC 660

TGGAATGAGC CTCTGTATCA TCTGGTCACG GAAGTACGTG GTATGCAAGA  
AGCCCCGGAG 720

GCTATCCTAT CCAAAGCTGT AGAGATTGAG GAGCAAACCA AATAAGTCGA C  
771

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGCTGAGGC GGCCTCCCCT ATGCTATCAC AACGGAGTTC AGTACAGAAA  
TAACGGTAAA 60

AGATCCCCGT GGTCATCTTG TTCTGTGACA TGTGGTGATG GTGTGATGGT



AAAAGAAGTG 120

GTACCCTGTA GACAAGACAG TGGACACCTC CTCCCCATTA A

161

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly Val Gln Tyr Arg  
1 5 10 15

Asn Asn Glu Glu Trp Thr Val Asp Ser Gly Lys Ser Ser Pro Trp Ser  
20 25 30

Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Gly Lys  
35 40 45

Ser Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val  
50 55 60

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCTGAGGC GGCCTCCCCT ATGCTATCAC AACGGAGTTC AGTACAGAAA  
TAACGGTAAA 60

AGATCCCCGT GGTCACTCTG TTCTGTGACA TGTGGTGATG GTGTGATGGT  
AAAAGAAGTG 120

GTACCCTGTA GACAAGACAG TGGACACCTC CTCCCCATTA TATTGGTTCT  
CGTGGTAAAA 180

GATAA

185

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TAGGTCTAGA ATGACTGAAG AGAACAAAGA G

31

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGGTCTAGA TTAGAGACGA CTACGTTTCT G

31

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Glu Ser Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu  
1 5 10 15

Thr Arg Ala Ala Ser Val Gly Leu Pro Gly Asp Phe Leu His Pro Pro  
20 25 30

Lys Leu Ser Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr  
35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro  
50 55 60

Asn Ala Gln Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly  
65 70 75 80

Gly Gly Asp Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val  
85 90 95

Gly Asn Asp Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile  
100 105 110

Ala Ser Thr Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile  
115 120 125

Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys  
130 135 140

Asn Lys Thr Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn  
145 150 155 160

Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly  
165 170 175

Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr  
180 185 190

Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp

195	200	205			
Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg					
210	215	220			
Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala					
225	230	235	240		
Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val					
245	250	255			
Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys					
260	265	270			
Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys					
275	280	285			
Met Phe Lys Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln					
290	295	300			
Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn					
305	310	315	320		
Arg Thr Phe Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser					
325	330	335			
Gly Met Lys Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile					
340	345	350			
Pro Val Lys Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg					
355	360	365			
Asn Gly Arg Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu					
370	375	380			
Leu Thr Ile Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val					
385	390	395	400		
Ile Leu Thr Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser					
405	410	415			
Leu Val Val Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser					
420	425	430			

Pro Met Asp Ser Tyr Gly Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr  
435 440 445

Val Tyr Ala Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu  
450 455 460

Glu Glu Ala Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys  
465 470 475 480

Lys Glu Trp Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu  
485 490 495

Val Thr Lys Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val  
500 505 510

Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys  
515 520 525

Glu Ala Ile Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His  
530 535 540

Val Ile Arg Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr  
545 550 555 560

Glu Gln Glu Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe  
565 570 575

Glu Asn Leu Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His  
580 585 590

Met Gly Glu Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp  
595 600 605

Lys Leu Asn Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile  
610 615 620

Val Ala Phe Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys  
625 630 635 640

Ser Ala Gln Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln  
645 650 655

Leu Ile Ile Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu  
660 665 670

Asn Gln Thr Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala  
675 680 685

Ser Gly Asn Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr  
690 695 700

Leu Val Glu Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu  
705 710 715 720

Thr Ile Arg Arg Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln  
725 730 735

Ala Cys Asn Val Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile  
740 745 750

Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly  
755 760 765

Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Leu Val  
770 775 780

Arg Thr Val Lys Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu  
785 790 795 800

Ser Ile Val Met Asp  
805

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGACGTCATG GAGAGCAAGG CGCTGCTAGC TGTCGCTCTG TGGTTCTGCG  
TGGAGACCCG 60

AGCCGCCTCT GTGGGTTTGC CTGGCGATTT TCTCCATCCC CCCAAGCTCA  
GCACACAGAA 120

AGACATACTG ACAATTTTGG CAAATACAAC CCTTCAGATT ACTTGCAGGG  
GACAGCGGGA 180

CCTGGACTGG CTTTGGCCCA ATGCTCAGCG TGATTCTGAG GAAAGGGTAT  
TGGTGAAGA 240

ATGCGGCGGT GGTGACAGTA TCTTCTGCAA AACACTCACC ATTCCCAGGG  
TGGTTGAAA 300

TGATACTGGA GCCTACAAGT GCTCGTACCG GGACGTCGAC ATAGCCTCCA  
CTGTTTATGT 360

CTATGTTCTGA GATTACAGAT CACCATTCTAT CGCCTCTGTC AGTGACCAGC  
ATGGCATCGT 420

GTACATCACC GAGAACAAGA ACAAACACTGT GGTGATCCCC TGCCGAGGGT  
CGATTTCAA 480

CCTCAATGTG TCTCTTTGCG CTAGGTATCC AGAAAAGAGA TTTGTTCCGG  
ATGGAAACAG 540

AATTTCTTGG GACAGCGAGA TAGGCTTTAC TCTCCCCAGT TACATGATCA  
GCTATGCCGG 600

CATGGTCTTC TGTGAGGCAA AGATCAATGA TGAAACCTAT CAGTCTATCA  
TGTACATAGT 660

TGTGGTTGTA GGATATAGGA TTTATGATGT GATTCTGAGC CCCCCGCATG  
AAATTGAGCT 720

ATCTGCCGGA GAAAAACTTG TCTTAAATTG TACAGCGAGA ACAGAGCTCA  
ATGTGGGGCT 780

TGATTTACAC TGGCACTCTC CACCTTCAA GTCTCATCAT AAGAAGATTG  
TAAACCGGGA 840

TGTGAAACCC TTTCTGGGA CTGTGGCGAA GATGTTTTTG AGCACCTTGA  
CAATAGAAAG 900

TGTGACCAAG AGTGACCAAG GGGAATACAC CTGTGTAGCG TCCAGTGGAC  
GGATGATCAA 960

GAGAAATAGA ACATTTGTCC GAGTTCACAC AAAGCCTTTT ATTGCTTTCG  
GTAGTGGGAT 1020

GAAATCTTTG GTGGAAGCCA CAGTGGGCAG TCAAGTCCGA ATCCCTGTGA  
AGTATCTCAG 1080

TTACCCAGCT CCTGATATCA AATGGTACAG AAATGGAAGG CCCATTGAGT  
CCAACTACAC 1140

AATGATTGTT GCGGATGAAC TCACCATCAT GGAAGTGAAGT GAAAGAGATG  
CAGGAAACTA 1200

CACGGTCATC CTCACCAACC CCATTTCAAT GGAGAAACAG AGCCACATGG  
TCTCTCTGGT 1260

TGTGAATGTC CCACCCCAGA TCGGTGAGAA AGCCTTGATC TCGCCTATGG  
ATTCCTACCA 1320

GTATGGGACC ATGCAGACAT TGACATGCAC AGTCTACGCC AACCTCCCC  
TGCACCACAT 1380

CCAGTGGTAC TGGCAGCTAG AAGAAGCCTG CTCCTACAGA CCCGGCCAAA  
CAAGCCCGTA 1440

TGCTTGTAAG GAATGGAGAC ACGTGGAGGA TTTCCAGGGG GGAAACAAGA  
TCGAAGTCAC 1500

CAAAAACCAA TATGCCCTGA TTGAAGGAAA AAACAAAACCT GTAAGTACGC  
TGGTCATCCA 1560

AGCTGCCAAC GTGTCAGCGT TGTACAAATG TGAAGCCATC AACAAAGCGG  
GACGAGGAGA 1620

GAGGGTCATC TCCTTCCATG TGATCAGGGG TCCTGAAATT ACTGTGCAAC  
CTGCTGCCCA 1680

GCCAACTGAG CAGGAGAGTG TGTCCCTGTT GTGCACTGCA GACAGAAATA  
CGTTTGAGAA 1740

CCTCACGTGG TACAAGCTTG GCTCACAGGC AACATCGGTC CACATGGGCG  
AATCACTCAC 1800

ACCAAGTTGC AAGAACTTGG ATGCTCTTTG GAAACTGAAT GGCACCATGT  
TTTCTAACAG 1860



CACAAATGAC ATCTTGATTG TGGCATTTC GAATGCCTCT CTGCAGGACC  
AAGGCGACTA 1920

TGTTTGCTCT GCTCAAGATA AGAAGACCAA GAAAAGACAT TGCCTGGTCA  
AACAGCTCAT 1980

CATCCTAGAG CGCATGGCAC CCATGATCAC CGGAAATCTG GAGAATCAGA  
CAACAACCAT 2040

TGGCGAGACC ATTGAAGTGA CTTGCCCAGC ATCTGGAAAT CCTACCCAC  
ACATTACATG 2100

GTTCAAAGAC AACGAGACCC TGGTAGAAGA TTCAGGCATT GTACTGAGAG  
ATGGGAACCG 2160

GAACCTGACT ATCCGCAGGG TGAGGAAGGA GGATGGAGGC CTCTACACCT  
GCCAGGCCTG 2220

CAATGTCCTT GGCTGTGCAA GAGCGGAGAC GCTCTTCATA ATAGAAGGTG  
CCCAGGAAAA 2280

GACCAACTTG GAAGTCATTA TCCTCGTCGG CACTGCAGTG ATTGCCATGT  
TCTTCTGGCT 2340

CCTTCTTGTC ATTCTCGTAC GGACCGTTAA GCGGGCCAAT GAAGGGGAAC  
TGAAGACAGG 2400

CTACTTGTCT ATTGTCATGG ATTAAGACGT C 2431

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	His	Thr	His	Gln	Asp	Phe	Gln	Pro	Val	Leu	His	Leu	Val	Ala	Leu
1		5		10		15									

Asn Thr Pro Leu Ser Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe  
20 25 30

Gln Cys Phe Asn Asn Ala Arg Val Gly Leu Ser Gly Thr Phe Arg Ala  
35 40 45

Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala  
50 55 60

Asp Arg Gly Ser Val Pro Ile Val Gln Asn Leu Arg Asp Glu Val Leu  
65 70 75 80

Ser Pro Ser Trp Asp Ser Leu Phe Ser Gly Ser Gln Gly Gln Leu Gln  
85 90 95

Pro Gly Ala Arg Ile Phe Ser Phe Asp Gly Arg Asp Val Leu Arg His  
100 105 110

Pro Ala Trp Pro Gln Arg Ser Val Trp His Gly Ser Asp Pro Ser Gly  
115 120 125

Arg Arg Leu Met Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Thr Thr  
130 135 140

Gly Ala Thr Gly Gln Ala Ser Ser Leu Leu Ser Gly Arg Leu Leu Glu  
145 150 155 160

Gln Arg Ala Ala Ser Cys His Asp Ser Tyr Ile Val Leu Cys Ile Glu  
165 170 175

Asn Ser Phe Met Thr Ser Phe Ser Arg  
180 185

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AGACGTCATG CATACTCATC AGGACTTTCA GCCAGTGCTC CACCTGGTGG  
CACTGAACAC 60

CCCCCTGTCT GGAGGCATGC GTGGTATCCG TGGAGCAGAT TTCCAGTGCT  
TCCAGCAAGC 120

CCGAGCCGTG GGGCTGTCTG GCACCTTCCG GGCTTTCCTG TCCTCTAGGC  
TGCAGGATCT 180

CTATAGCATC GTGCGCCGTG CTGACCGGGG GTCTGTGCCC ATCGTCAACC  
TGAAGGACGA 240

GGTGCTATCT CCCAGCTGGG ACTCCCTGTT TTCTGGCTCC CAGGGTCAAC  
TGCAACCCGG 300

GGCCCGCATC TTTTCTTTTG ACGGCAGAGA TGTCTGAGA CACCCAGCCT  
GGCCGCAGAA 360

GAGCGTATGG CACGGCTCGG ACCCCAGTGG GCGGAGGCTG ATGGAGAGTT  
ACTGTGAGAC 420

ATGGCGAACT GAAACTACTG GGGCTACAGG TCAGGCCTCC TCCCTGCTGT  
CAGGCAGGCT 480

CCTGGAACAG AAAGCTGCGA GCTGCCACAA CAGCTACATC GTCCTGTGCA  
TTGAGAATAG 540

CTTCATGACC TCTTTCTCCA AATAG 565

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTATCGTCGA CATGTATATT GGTTCGTT AAGTCGACCT ATC

43

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATAGGTCGA CTTAACGAGA ACCAATATAC ATGTCGACGA TAG

43

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGTATCTAGA ATGAGTGTAT CTGTCACAAT G

31

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAATTCTAGA TCACCTATGA GGGGTTTGCT C

31

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTATCGTCGA CATGTATATT GGTTCGTA AAAGATATAT TGGTTCTCGT  
GGTAAAAGAG 60

ATGGTTCTCG TGGTAAAAGA TAAGTGACCT ATC

93

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATAGGTCGA CTTAT

15